

RAW SEQUENCE LISTING  
PATENT APPLICATION US/10/734,126DATE: 08/30/2004  
TIME: 14:17:48*pages 1-5 shown.*

INPUT SET: S30662.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information:  
4 (i) APPLICANT: Plowman, Gregory  
5 Mossie, Kevin  
6 (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1  
7 AND/OR AUR-2 RELATED DISORDERS  
8 (iii) NUMBER OF SEQUENCES: 39  
9 (iv) CORRESPONDENCE ADDRESS:  
10 (A) ADDRESSEE: Lyon & Lyon  
11 (B) STREET: 633 West Fifth Street  
12 Suite 4700  
13 (C) CITY: Los Angeles  
14 (D) STATE: California  
15 (E) COUNTRY: U.S.A.  
16 (F) ZIP: 90071-2066  
17 (v) COMPUTER READABLE FORM:  
18 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
19 storage  
20 (B) COMPUTER: IBM Compatible  
21 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
22 (D) SOFTWARE: FastSEQ for Windows 2.0  
23 (vi) CURRENT APPLICATION DATA:  
24 (A) APPLICATION NUMBER: US/10/734,126  
25 (B) FILING DATE: 15-Dec-2003  
26 (C) CLASSIFICATION: <Unknown>  
27 (vii) PRIOR APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US/09/784,332  
29 (B) FILING DATE: 16-Feb-2001  
30  
31 (viii) PRIOR APPLICATION DATA:  
32 (A) APPLICATION NUMBER: 09/283,011  
33 (B) FILING DATE: <Unknown>  
34 (A) APPLICATION NUMBER: 09/012,135  
35 (B) FILING DATE: January 22, 1998  
36 (A) APPLICATION NUMBER: 08/755,728  
37 (B) FILING DATE: November 25, 1996  
38 (A) APPLICATION NUMBER: 60/023,943  
39 (B) FILING DATE: August 14, 1996  
40 (A) APPLICATION NUMBER: 60/008,809  
41 (B) FILING DATE: December 18, 1995  
42 (ix) ATTORNEY/AGENT INFORMATION:  
43 (A) NAME: Warburg, Richard J.  
44 (B) REGISTRATION NUMBER: 32,327  
45 (C) REFERENCE/DOCKET NUMBER: 231/282  
46 (x) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: (213) 489-1600  
48 (B) TELEFAX: (213) 955-0440  
49 (C) TELEX: 67-3510  
50 (2) INFORMATION FOR SEQ ID NO: 1:  
51 (i) SEQUENCE CHARACTERISTICS:  
52 (A) LENGTH: 1244 base pairs  
53 (B) TYPE: nucleic acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear  
56 (ii) MOLECULE TYPE: cDNA  
57 (iii) HYPOTHETICAL: NO  
58 (iv) ANTI-SENSE: NO  
59 (vi) ORIGINAL SOURCE:  
60 (A) ORGANISM: Homo sapiens  
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
62 CGGGAGAGTA GCAGTGCCCTT GGACCCCAGC TCTCCTCCCC CTTTCTCTCT AAGGATGGCC 60  
63 CAGAAGGAGA ACTCCTACCC CTGGCCCTAC GGCCGACAGA CGGCTCCATC TGGCCTGAGC 120  
64 ACCCTGCCCC AGCGAGTCCT CCGGAAAGAG CCTGTCACCC CATCTGCACT TGTCCTCATG 180  
65 AGCCGCTCCA ATGTCCAGCC CACAGCTGCC CCTGGCCAGA AGGTGATGGA GAATAGCAGT 240  
66 GGGACACCCG ACATCTTAAC GCGGCACCTC ACAATTGATG ACTTTGAGAT TGGGCGTCTT 300  
67 CTGGGCAAAG GCAAGTTTGG AAACGTGTAC TTGGCTCGGG AGAAGAAAAG CCATTTTCATC 360  
68 GTGGCGCTCA AGGTCTCTCT CAAGTCCAG ATAGAGAAGG AGGGCGTGGA GCATCAGCTG 420  
69 CGCAGAGAGA TCGAAATCCA GGCCACCTG CACCATCCCA ACATCCTGCG TCTCTACAAC 480  
70 TATTTTTATG ACCGGAGGAG GATCTACTTG ATTCTAGAGT ATGCCCCCG CGGGGAGCTC 540  
71 TACAAGGAGC TGCAGAAGAG CTGCACATTT GACGAGCAGC GAACAGCCAC GATCATGGAG 600  
72 GAGTTGGCAG ATGCTCTAAT GTACTGCCAT GGGAGAAGG TGATTACAG AGACATAAAG 660  
73 CCAGAAAATC TGCTCTTAGG GCTCAAGGGA GAGCTGAAGA TTGCTGACTT CGGCTGGTCT 720  
74 GTGCATGCGC CCTCCCTGAG GAGGAAGACA ATGTGTGGCA CCCTGGACTA CCTGCCCCCA 780  
75 GAGATGATTG AGGGGCGCAT GCACAATGAG AAGGTGGATC TGTGGTGAT TGGAGTGCTT 840  
76 TGCTATGAGC TGCTGGTGGG GAACCCACCC TTCGAGAGTG CATCACACAA CGAGACCTAT 900  
77 CGCCGCATCG TCAAGGTGGA CCTAAAGTTC CCCGCTTCTG TGCCACGGG AGCCCAGGAC 960  
78 CTCATCTCCA AACTGCTCAG GCATAACCC TCGGAACGGC TGCCCTGGC CCAGGTCTCA 1020  
79 GCCCACCTT GGGTCCGGG CAACTCTCG AGGGTGCTGC CTCCCTCTGC CCTTCAATCT 1080  
80 GTCGCTGAT GGTCCCTGTC ATTCACTCG GTGCGTGTGT TTGTATGTCT GTGTATGTAT 1140  
81 AGGGGAAAGA AGGGATCCCT AACTGTTCCC TTATCTGTTT TCTACCTCCT CCTTTGTTTA 1200  
82 ATAAAGGCTG AAGCTTTTTG TAAAAAACA AAAAAAAAAA AAAA 1244  
83  
84 (2) INFORMATION FOR SEQ ID NO: 2:  
85 (i) SEQUENCE CHARACTERISTICS:  
86 (A) LENGTH: 2198 base pairs  
87 (B) TYPE: nucleic acid  
88 (C) STRANDEDNESS: single  
89 (D) TOPOLOGY: linear  
90 (ii) MOLECULE TYPE: cDNA  
91 (iii) HYPOTHETICAL: NO  
92 (iv) ANTI-SENSE: NO  
93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
94 GGGATATCTC AGTGGCGGAC GAGGACGGCG GGGACAAGGG GCGGCTGGTC GGAGTGGCGG 60  
95 ACGTCAAGTC CCCTGTCGGT TCCTCCGTCC CTGAGTGTCC TTGGCGCTGC CTTGTGCCCC 120  
96 CCCAGCGCCT TTGCATCCGC TCCTGGGCAC CGAGGCGCCC TGTAGGATAC TGCTTGTTAC 180  
97 TTATTACAGC TAGAGGCATC ATGGACCGAT CTAAAGAAAA CTGCATTTCA GGACCTGTTA 240  
98 AGGCTACAGC TCCAGTTGGA GGTCCAAAAC GTGTTCTCGT GACTCAGCAA TTTCCCTGTG 300  
99 AGAATCCATT ACCTGTAAAT AGTGGCCAGG CTCAGCGGGT CTTGTGTCCT TCAAAATCTT 360

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100	CCCAGCGCGT	TCCTTTGCAA	GCACAAAAGC	TTGTCTCCAG	TCACAAGCCG	GTTCAGAATC	420
101	AGAAGCAGAA	GCAATTGCAG	GCAACCAGTG	TACCTCATCC	TGTCTCCAGG	CCACTGAATA	480
102	ACACCCAAAA	GAGCAAGCAG	CCCCTGCCAT	CGGCACCTGA	AAATAATCCT	GAGGAGGAAC	540
103	TGGCATCAAA	ACAGAAAAAT	GAAGAATCAA	AAAAGAGGCA	GTGGGCTTTG	GAAGACTTTG	600
104	AAATTGGTGC	CCCTCTGGGT	AAAGGAAAGT	TTGGTAATGT	TTATTTGGCA	AGAGAAAAGC	660
105	AAAGCAAGTT	TATTCTGGCT	CTTAAAGTGT	TATTTAAAGC	TCAGCTGGAG	AAAGCCGGAG	720
106	TGGAGCATCA	GCTCAGAAGA	GAAGTAGAAA	TACAGTCCCA	CCTTCGGCAT	CCTAATATTC	780
107	TTAGACTGTA	TGGTTATTTT	CATGATGCTA	CCAGAGTCTA	CCTAATTCTG	GAATATGCAC	840
108	CACTTGGAAC	AGTTTATAGA	GAACCTCAGA	AACTTTCAAA	GTTTGATGAG	CAGAGAACTG	900
109	CTACTTATAT	AACAGAAATG	GCAAATGCCC	TGCTTTACTG	TCATTCTGAAG	AGAGTTATTC	960
110	ATAGAGACAT	TAAGCCAGAG	AACTTACTTC	TTGGATCAGC	TGGAGAGCTT	AAAATTGCAG	1020
111	ATTTTGGGTG	GTCAGTACAT	GCTCCATCTT	CCAGGAGGAC	CACCTCTCTG	GGCACCCCTG	1080
112	ACTACCTGCC	CCCTGAAATG	ATTGAAGGTC	GGATGCATGA	TGAGAAGGTG	GATCTCTGGA	1140
113	GCCTTGGAGT	TCTTTGCTAT	GAATTTTATG	TTGGGAAGCC	TCCTTTTGAG	GCAAACACAT	1200
114	ACCAAGAGAC	CTACAAAAGA	ATATCACGGG	TTGAATTCAC	ATTCCCTGAC	TTTGTAACAG	1260
115	AGGGAGCCAG	GGACCTCATT	TCAAGACTGT	TGAAGCATAA	TCCCAGCCAG	AGGCCAATGC	1320
116	TCAGAGAAGT	ACTTGAACAC	CCCTGGATCA	CAGCAAATTC	ATCAAAACCA	TCAAATTGCC	1380
117	AAAACAAAGA	ATCAGCTAGC	AAACAGTCTT	AGGAATCGTG	CAGGGGGAGA	AATCCTTGAG	1440
118	CCAGGGCTGC	CATATAACCT	GACAGGAACA	TGCTACTGAA	GTTTATTTTA	CCATTGACTG	1500
119	CTGCCCCTAA	TCTAGAACGC	TACACAAGAA	ATATTTGTTT	TACTCAGCAG	GTGTGCCTTA	1560
120	ACCTCCCTAT	TCAGAAAGCT	CCACATCAAT	AAACATGACA	CTCTGAAGTG	AAAGTAGCCA	1620
121	CGAGAATTGT	GCTACTTATA	CTGGTTCATA	ATCTGGAGGC	AAGGTTTCGAC	TGCAGCCGCC	1680
122	CCGTCAGCCT	GTGCTAGGCA	TGGTGTCTTC	ACAGGAGGCA	AATCCAGAGC	CTGGCTGTGG	1740
123	GGAAAGTGAC	CACCTCTGCC	TGACCCCGAT	CAGTTAAGGA	GCTGTGCAAT	AACCTTCCTA	1800
124	GTACCTGAGT	GAGTGTGTAA	CTTATTGGGT	TGGCGAAGCC	TGGTAAAGCT	GT'TGGAATGA	1860
125	GTATGTGATT	CTTTTAAAGT	ATGAAAATAA	AGATATATGT	ACAGACTTGT	ATTTTTCCTC	1920
126	TGGTGGCATT	CCTTTAGGAA	TGCTGTGTGT	CTGTCCGGCA	CCCCGGTAGG	CCTGATTGGG	1980
127	TTTCTAGTCC	TCCTTAACCA	CTTATCTCCC	ATATGAGAGT	GTGAAAATAA	GGAACACGTG	2040
128	CTCTACCTCC	ATTTAGGGAT	TTGCTTGGGA	TACAGAAGAG	GCCATGTGTC	TCAGAGCTGT	2100
129	TAAGGGCTTA	TTTTTTTAAA	ACATTGGAGT	CATAGCATGT	GTGTAAACTT	TAAATATGCA	2160
130	AATAAATAAG	TATCTATGTC	AAAAAAAAAA	AAAAAAAAAA			2198

## (2) INFORMATION FOR SEQ ID NO: 3:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (iii) HYPOTHETICAL: NO

### (iv) ANTI-SENSE: NO

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

142	Met	Ala	Gln	Lys	Glu	Asn	Ser	Tyr	Pro	Trp	Pro	Tyr	Gly	Arg	Gln	Thr
143	1				5					10					15	
144	Ala	Pro	Ser	Gly	Leu	Ser	Thr	Leu	Pro	Gln	Arg	Val	Leu	Arg	Lys	Glu
145				20					25					30		
146	Pro	Val	Thr	Pro	Ser	Ala	Leu	Val	Leu	Met	Ser	Arg	Ser	Asn	Val	Gln
147			35					40					45			
148	Pro	Thr	Ala	Ala	Pro	Gly	Gln	Lys	Val	Met	Glu	Asn	Ser	Ser	Gly	Thr
149		50				55					60					
150	Pro	Asp	Ile	Leu	Thr	Arg	His	Phe	Thr	Ile	Asp	Asp	Phe	Glu	Ile	Gly
151	65				70					75				80		
152	Arg	Pro	Leu	Gly	Lys	Gly	Lys	Phe	Gly	Asn	Val	Tyr	Leu	Ala	Arg	Glu

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153                               85                               90                               95
154      Lys Lys Ser His Phe Ile Val Ala Leu Lys Val Leu Phe Lys Ser Gln
155                               100                               105                               110
156      Ile Glu Lys Glu Gly Val Glu His Gln Leu Arg Arg Glu Ile Glu Ile
157                               115                               120                               125
158      Gln Ala His Leu His His Pro Asn Ile Leu Arg Leu Tyr Asn Tyr Phe
159                               130                               135                               140
160      Tyr Asp Arg Arg Arg Ile Tyr Leu Ile Leu Glu Tyr Ala Pro Arg Gly
161      145                               150                               155                               160
162      Glu Leu Tyr Lys Glu Leu Gln Lys Ser Cys Thr Phe Asp Glu Gln Arg
163                               165                               170                               175
164      Thr Ala Thr Ile Met Glu Glu Leu Ala Asp Ala Leu Met Tyr Cys His
165                               180                               185                               190
166      Gly Lys Lys Val Ile His Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu
167                               195                               200                               205
168      Gly Leu Lys Gly Glu Leu Lys Ile Ala Asp Phe Gly Trp Ser Val His
169                               210                               215                               220
170      Ala Pro Ser Leu Arg Arg Lys Thr Met Cys Gly Thr Leu Asp Tyr Leu
171      225                               230                               235                               240
172      Pro Pro Glu Met Ile Glu Gly Arg Met His Asn Glu Lys Val Asp Leu
173                               245                               250                               255
174      Trp Cys Ile Gly Val Leu Cys Tyr Glu Leu Leu Val Gly Asn Pro Pro
175                               260                               265                               270
176      Phe Glu Ser Ala Ser His Asn Glu Thr Tyr Arg Arg Ile Val Lys Val
177                               275                               280                               285
178      Asp Leu Lys Phe Pro Ala Ser Val Pro Thr Gly Ala Gln Asp Leu Ile
179      290                               295                               300
180      Ser Lys Leu Leu Arg His Asn Pro Ser Glu Arg Leu Pro Leu Ala Gln
181      305                               310                               315                               320
182      Val Ser Ala His Pro Trp Val Arg Ala Asn Ser Arg Arg Val Leu Pro
183                               325                               330                               335
184      Pro Ser Ala Leu Gln Ser Val Ala
185                               340
186

```

## (2) INFORMATION FOR SEQ ID NO: 4:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (iii) HYPOTHETICAL: NO

### (iv) ANTI-SENSE: NO

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

197      Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala Thr
198      1                               5                               10                               15
199      Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Phe Pro
200      20                               25                               30
201      Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
202      35                               40                               45
203      Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
204      50                               55                               60
205      Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln

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206	65				70				75				80			
207	Ala	Thr	Ser	Val	Pro	His	Pro	Val	Ser	Arg	Pro	Leu	Asn	Asn	Thr	Gln
208					85					90					95	
209	Lys	Ser	Lys	Gln	Pro	Leu	Pro	Ser	Ala	Pro	Glu	Asn	Asn	Pro	Glu	Glu
210				100					105					110		
211	Glu	Leu	Ala	Ser	Lys	Gln	Lys	Asn	Glu	Glu	Ser	Lys	Lys	Arg	Gln	Trp
212				115					120					125		
213	Ala	Leu	Glu	Asp	Phe	Glu	Ile	Gly	Arg	Pro	Leu	Gly	Lys	Gly	Lys	Phe
214				130				135					140			
215	Gly	Asn	Val	Tyr	Leu	Ala	Arg	Glu	Lys	Gln	Ser	Lys	Phe	Ile	Leu	Ala
216	145					150					155				160	
217	Leu	Lys	Val	Leu	Phe	Lys	Ala	Gln	Leu	Glu	Lys	Ala	Gly	Val	Glu	His
218					165					170					175	
219	Gln	Leu	Arg	Arg	Glu	Val	Glu	Ile	Gln	Ser	His	Leu	Arg	His	Pro	Asn
220				180					185					190		
221	Ile	Leu	Arg	Leu	Tyr	Gly	Tyr	Phe	His	Asp	Ala	Thr	Arg	Val	Tyr	Leu
222				195				200						205		
223	Ile	Leu	Glu	Tyr	Ala	Pro	Leu	Gly	Thr	Val	Tyr	Arg	Glu	Leu	Gln	Lys
224			210				215					220				
225	Leu	Ser	Lys	Phe	Asp	Glu	Gln	Arg	Thr	Ala	Thr	Tyr	Ile	Thr	Glu	Leu
226	225					230					235				240	
227	Ala	Asn	Ala	Leu	Ser	Tyr	Cys	His	Ser	Lys	Arg	Val	Ile	His	Arg	Asp
228					245					250					255	
229	Ile	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Gly	Ser	Ala	Gly	Glu	Leu	Lys	Ile
230				260					265					270		
231	Ala	Asp	Phe	Gly	Trp	Ser	Val	His	Ala	Pro	Ser	Ser	Arg	Arg	Thr	Thr
232			275					280					285			
233	Leu	Cys	Gly	Thr	Leu	Asp	Tyr	Leu	Pro	Pro	Glu	Met	Ile	Glu	Gly	Arg
234		290				295						300				
235	Met	His	Asp	Glu	Lys	Val	Asp	Leu	Trp	Ser	Leu	Gly	Val	Leu	Cys	Tyr
236	305					310					315				320	
237	Glu	Phe	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Ala	Asn	Thr	Tyr	Gln	Glu
238					325					330					335	
239	Thr	Tyr	Lys	Arg	Ile	Ser	Arg	Val	Glu	Phe	Thr	Phe	Pro	Asp	Phe	Val
240				340					345					350		
241	Thr	Glu	Gly	Ala	Arg	Asp	Leu	Ile	Ser	Arg	Leu	Leu	Lys	His	Asn	Pro
242			355				360						365			
243	Ser	Gln	Arg	Pro	Met	Leu	Arg	Glu	Val	Leu	Glu	His	Pro	Trp	Ile	Thr
244		370					375					380				
245	Ala	Asn	Ser	Ser	Lys	Pro	Ser	Asn	Cys	Gln	Asn	Lys	Glu	Ser	Ala	Ser
246	385					390					395				400	
247	Lys	Gln	Ser													
248																

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln

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